



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 157552

TO: Nita M Minnifield  
Location: rem/3C01/3C18  
Art Unit: 1645  
Thursday, June 30, 2005

Case Serial Number: 09/196161

From: Noble Jarrell  
Location: Biotech-Chem Library  
Rem 1B71  
Phone: 272-2556

Noble.jarrell@uspto.gov

### Search Notes

*Reviewed  
7-1-05  
M*

STIC-Biotech/ChemLib

157552

mej

From: Chan, Christina  
Sent: Monday, June 27, 2005 10:14 AM  
To: Minnifield, Nita; STIC-Biotech/ChemLib  
Subject: RE: rush sequence search

Please ~~rush~~. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

RECEIVED  
JUN 27 2005  
(STIC)

-----Original Message-----

From: Minnifield, Nita  
Sent: Sunday, June 26, 2005 10:00 AM  
To: Chan, Christina  
Subject: rush sequence search

Christina,  
Please approve, 2 month amdt. due.  
Thanks,  
Minnifield

STIC

09/196161

Please do a commercial and interference sequence search on SEQ ID NO: 1 of this application.

Please search both aa and nt databases.

Please provide a paper copy of the results.

Thanks,  
Minnifield,  
71976  
Art Unit 1645  
Office REM-3C01  
Mailbox REM-3C18

\*\*\*\*\*

STAFF USE ONLY

Searcher: Noble  
Searcher Phone: 2-  
Date Searcher Picked up: 6/23/05  
Date Completed: 5  
Searcher Prep/Rev. Time: 5  
Online Time: 5

\*\*\*\*\*

Type of Search

NA#: 1 AA#: 1  
Interference: ✓ SPDI:      
S/L:     Oligomer:      
Encode/Transl:      
Structure#:     Text:      
Inventor:     Litigation:    

\*\*\*\*\*

Vendors and cost where applicable

STN:      
DIALOG:      
QUESTEL/ORBIT:      
LEXIS/NEXIS:      
SEQUENCE SYSTEM: Campana  
WWW/Internet:      
Other(Specify):

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 05:17:22 ; Search time 2572 Seconds  
(without alignments)  
256.057 Million cell updates/sec

Title: US-09-196-161D-1

Perfect score: 558

Sequence: 1 GAAAGGANGQPPANNAAR.....PGGAPGVYFAAGAAAGV 105

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 631374 segs, 3136092125 residues  
Total number of hits satisfying chosen parameters: 12626748

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_plus\_p2n.model -DEV=xlh  
-G=/cgn2\_1/USPTO.spool\_h/US09196161/runat\_28062005\_090809\_20882/app\_query.fasta\_1.263  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsun62  
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09196161 @CGN\_1\_1\_460 @runat\_28062005\_090809\_20882  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-YGAPOP=6 -YGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
Published Applications NA:  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:  
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16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:  
18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:  
19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:  
20: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq:  
21: /cgn2\_6/ptodata/2/pubpna/US10J\_PUBCOMB.seq:  
22: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:  
23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:  
24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:  
25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:  
26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length  | DB ID | Description          |
|------------|-------|-------------|---------|-------|----------------------|
| 1          | 495   | 88.7        | 1326    | 21    | US-10-878-694-7      |
| 2          | 495   | 88.7        | 2811    | 21    | US-10-878-694-3      |
| 3          | 495   | 88.7        | 2811    | 21    | US-10-878-694-8      |
| 4          | 212   | 38.0        | 1404    | 21    | US-10-878-694-8      |
| 5          | 84.5  | 15.1        | 4355    | 18    | US-10-263-929-95     |
| 6          | 84.5  | 15.1        | 5216    | 18    | US-10-263-929-95     |
| 7          | 84.5  | 15.1        | 6056    | 18    | US-10-466-720-21     |
| 8          | 84.5  | 15.1        | 7244    | 17    | US-10-120-988-143    |
| 9          | 84.5  | 15.1        | 8589    | 17    | US-10-085-198-15     |
| 10         | 84    | 15.1        | 2335    | 9     | US-09-996-620-9      |
| 11         | 84    | 15.1        | 2359    | 9     | US-09-996-620-17     |
| 12         | 83    | 14.9        | 3989    | 15    | US-10-053-662A-1     |
| 13         | 82    | 14.7        | 669     | 18    | US-10-424-599-139576 |
| 14         | 80.5  | 14.4        | 783     | 17    | US-10-282-122A-13344 |
| 15         | 80.5  | 14.4        | 1834    | 18    | US-10-425-114-32066  |
| 16         | 80.5  | 14.4        | 2023    | 20    | US-10-425-115-54885  |
| 17         | 80    | 14.3        | 624     | 13    | US-10-027-632-220391 |
| 18         | 80    | 14.3        | 624     | 17    | US-10-027-632-220391 |
| 19         | 80    | 14.3        | 6425    | 19    | US-10-322-281-350    |
| 20         | 79    | 14.2        | 969     | 19    | US-10-437-963-50968  |
| 21         | 79    | 14.2        | 2388    | 13    | US-10-029-180-51     |
| 22         | 79    | 14.2        | 2388    | 21    | US-10-952-045-51     |
| 23         | 79    | 14.2        | 8077    | 21    | US-10-764-420-2784   |
| 24         | 78    | 14.0        | 11009   | 9     | US-09-845-583-1      |
| 25         | 78    | 14.0        | 11009   | 14    | US-10-037-182-3      |
| 26         | 78    | 14.0        | 11009   | 21    | US-10-764-420-947    |
| 27         | 78    | 14.0        | 9025608 | 15    | US-10-156-761-1      |
| 28         | 77.5  | 13.9        | 929     | 20    | US-10-653-047-7620   |
| 29         | 77.5  | 13.9        | 1213    | 9     | US-09-921-823-1      |
| 30         | 77.5  | 13.9        | 1722    | 18    | US-10-389-647-247    |
| 31         | 77.5  | 13.8        | 1328    | 21    | US-10-825-692-11     |
| 32         | 77    | 13.8        | 3657    | 19    | US-10-437-963-16526  |
| 33         | 77    | 13.8        | 6130    | 9     | US-09-970-318-3      |
| 34         | 77    | 13.8        | 11558   | 10    | US-09-949-029-133    |
| 35         | 76.5  | 13.7        | 3057    | 18    | US-10-263-929-94     |
| 36         | 76    | 13.6        | 5113    | 17    | US-10-603-725-11     |
| 37         | 76    | 13.6        | 5264    | 17    | US-10-603-725-9      |
| 38         | 76    | 13.6        | 6442    | 19    | US-10-437-963-16526  |
| 39         | 75.5  | 13.5        | 386     | 18    | US-10-424-599-130425 |
| 40         | 75.5  | 13.5        | 646     | 21    | US-10-487-901-1775   |
| 41         | 75.5  | 13.5        | 646     | 21    | US-10-487-901-4220   |
| 42         | 75.5  | 13.5        | 701     | 13    | US-10-027-632-125233 |
| 43         | 75.5  | 13.5        | 701     | 17    | US-10-027-632-125233 |
| 44         | 75.5  | 13.5        | 519599  | 22    | US-10-737-082-73     |
| 45         | 75.5  | 13.5        | 519599  | 22    | US-10-765-790-73     |

## ALIGNMENTS

RESULT 1  
US-10-878-694-7  
Sequence 7, Application US/10878694  
Publication No. US20050106164A1  
GENERAL INFORMATION:  
APPLICANT: GARRIG, Jacek  
APPLICANT: DICKERSON Jr., Harry W.  
APPLICANT: CLARK, Theodore G.  
TITLE OF INVENTION: THE UNIVERSITY OF GEORGIA RESEARCH FOUNDATION INC  
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN  
FILE REFERENCE: 235, 00100101  
CURRENT APPLICATION NUMBER: US/10/878,694  
PRIOR FILING DATE: 2004-06-28  
PRIOR APPLICATION NUMBER: US/09/498,612  
PRIOR FILING DATE: 2000-02-04

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 04:01:43 / Search time 155 Seconds  
(without alignments)  
1108.446 Million cell updates/sec

Title: US-09-196-161D-1  
Perfect score: 558  
Sequence: 1 GAAOGEANGNCPFAANNAR.....POGEAPGVVPAAGAAAGV 105

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1202784 segs, 818138359 residues  
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame\_plus\_p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO\_spool\_h/US09196161/rnatec\_28062005\_090807\_20808/app\_query.fasta\_1.263  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rm1 -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*

- 1: /cgn2\_6/prodata/1/ina/5A.COMB.seq:\*
- 2: /cgn2\_6/prodata/1/ina/5B.COMB.seq:\*
- 3: /cgn2\_6/prodata/1/ina/6A.COMB.seq:\*
- 4: /cgn2\_6/prodata/1/ina/6B.COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/PCUTS.COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/Backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                            |
|------------|-------|-------------|--------|----|--|
| 1          | 84.5  | 15.1        | 7244   | 4  | US-09-774-528-143 Sequence 143, App    |
| 2          | 84    | 15.1        | 2335   | 3  | US-09-026-001A-9 Sequence 9, Appl      |
| 3          | 84    | 15.1        | 2359   | 3  | US-09-026-001A-17 Sequence 17, Appl    |
| 4          | 79    | 14.2        | 2388   | 4  | US-10-029-180-51 Sequence 51, Appl     |
| 5          | 78    | 14.0        | 11009  | 4  | US-09-845-583A-1 Sequence 1, Appl      |
| 6          | 77.5  | 13.9        | 996    | 4  | US-09-252-991A-11818 Sequence 11818, A |
| 7          | 77.5  | 13.9        | 1545   | 4  | US-09-252-991A-11565 Sequence 11565, A |
| 8          | 77.5  | 13.9        | 2589   | 4  | US-09-252-991A-11884 Sequence 11884, A |
| 9          | 77.5  | 13.9        | 11220  | 4  | US-09-949-016-5061 Sequence 5061, Ap   |
| 10         | 77    | 13.8        | 1320   | 4  | US-08-419-414-1 Sequence 1, Appl       |
| 11         | 77    | 13.8        | 6330   | 4  | US-09-949-016-914 Sequence 914, App    |
| 12         | 76    | 13.6        | 5113   | 4  | US-09-560-385A-11 Sequence 11, Appl    |

|    |      |      |         |   |                     |                   |
|----|------|------|---------|---|---------------------|-------------------|
| 13 | 76   | 13.6 | 5264    | 4 | US-09-560-385A-9    | Sequence 9, Appl  |
| 14 | 75   | 13.4 | 3620    | 4 | US-09-560-385A-31   | Sequence 31, Appl |
| 15 | 75   | 13.4 | 3720    | 4 | US-09-560-385A-29   | Sequence 29, Appl |
| 16 | 75   | 13.4 | 4316    | 1 | US-08-317-450B-14   | Sequence 14, Appl |
| 17 | 75   | 13.4 | 4316    | 3 | US-08-800-593-14    | Sequence 14, Appl |
| 18 | 75   | 13.4 | 4316    | 3 | US-09-560-385A-27   | Sequence 27, Appl |
| 19 | 75   | 13.4 | 5020    | 4 | US-09-643-597-130   | Sequence 130, App |
| 20 | 75   | 13.4 | 5156    | 3 | US-09-480-884A-130  | Sequence 130, App |
| 21 | 75   | 13.4 | 5156    | 4 | US-09-542-615A-130  | Sequence 130, App |
| 22 | 75   | 13.4 | 5156    | 4 | US-09-606-421B-130  | Sequence 130, App |
| 23 | 75   | 13.4 | 5156    | 4 | US-09-221-107-130   | Sequence 130, App |
| 24 | 75   | 13.4 | 5156    | 4 | US-09-466-396A-130  | Sequence 130, App |
| 25 | 75   | 13.4 | 5156    | 4 | US-09-476-496A-130  | Sequence 130, App |
| 26 | 75   | 13.4 | 5156    | 4 | US-09-630-940B-130  | Sequence 130, App |
| 27 | 75   | 13.4 | 5156    | 4 | US-09-285-479-130   | Sequence 130, App |
| 28 | 75   | 13.4 | 5200    | 1 | US-08-317-450B-12   | Sequence 12, Appl |
| 29 | 75   | 13.4 | 5200    | 3 | US-08-800-593-12    | Sequence 12, Appl |
| 30 | 75   | 13.4 | 5200    | 4 | US-09-560-385A-25   | Sequence 25, Appl |
| 31 | 74   | 13.3 | 28055   | 4 | US-09-949-016-16441 | Sequence 16441, A |
| 32 | 73.5 | 13.2 | 468     | 3 | US-08-600-982-29    | Sequence 29, Appl |
| 33 | 73.5 | 13.2 | 468     | 5 | PCP-US94-10261A-29  | Sequence 29, Appl |
| 34 | 73.5 | 13.2 | 846     | 4 | US-09-902-540-8701  | Sequence 8701, Ap |
| 35 | 73.5 | 13.2 | 915     | 4 | US-09-489-039A-4735 | Sequence 4735, Ap |
| 36 | 73.5 | 13.2 | 5170    | 4 | US-09-560-385A-3    | Sequence 3, Appl  |
| 37 | 73.5 | 13.2 | 5280    | 4 | US-09-560-385A-1    | Sequence 1, Appl  |
| 38 | 73.5 | 13.2 | 5373    | 4 | US-09-560-385A-7    | Sequence 7, Appl  |
| 39 | 73.5 | 13.2 | 5433    | 4 | US-09-560-385A-5    | Sequence 5, Appl  |
| 40 | 73.5 | 13.2 | 5496    | 3 | US-08-600-982-23    | Sequence 23, Appl |
| 41 | 73.5 | 13.2 | 5496    | 5 | PCP-US94-10261A-23  | Sequence 23, Appl |
| 42 | 73.5 | 13.2 | 7109    | 4 | US-09-902-540-922   | Sequence 922, App |
| 43 | 73   | 13.1 | 2310    | 4 | US-09-489-039A-5030 | Sequence 5030, Ap |
| 44 | 73   | 13.1 | 4403765 | 3 | US-09-103-840A-2    | Sequence 2, Appl  |
| 45 | 73   | 13.1 | 4411529 | 3 | US-09-103-840A-1    | Sequence 1, Appl  |

ALIGNMENTS

RESULT 1  
US-09-774-528-143  
Sequence 143, Application US/09774528  
Patent No. 6743619  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Zhou, Ping  
APPLICANT: Goodrich, Ryle  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Ren, Feiyan  
APPLICANT: Zhang, Jie  
APPLICANT: Zhao, Qing A.  
APPLICANT: Yang, Yonghong  
APPLICANT: Xue, Aidong J.  
APPLICANT: Wehrman, Tom  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Wang, Dunrui  
APPLICANT: Dimenac, Radoje T.  
TITLE OF INVENTION: No. 6743619el Nucleic Acids and  
FILE REFERENCE: 802 Polypeptides  
CURRENT APPLICATION NUMBER: US/09/774,528  
CURRENT FILING DATE: 2001-01-30  
NUMBER OF SEQ ID NOS: 441  
SOFTWARE: pc\_fl\_genes Version 2.0  
SEQ ID NO 143  
LENGTH: 7244  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (714)..(6518)  
US-09-774-528-143  
Alignment Scores:

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 03:54:37 ; Search time 453 Seconds  
(without alignments)  
1372.125 Million cell updates/sec

Title: US-09-196-161D-1

Perfect score: 558

Sequence: 1 GAAAGANGNPPANNAAR.....PGAPGVVFAAGAAAGV 105

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4390206 segs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh  
-Q=cm2.1/USPTO.spool.h/US09196161/runat.28062005.090805.20776/app.query.fasta.1.263  
-DB=N.Geneseg -QMT=fastcap -SUFFIX=mg -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTPRT=pco -NORM=exc -HEA=SIZE=500 -MINLEN=50 -MAXLEN=2000000000  
-USER=US09196161.0CCN.1.1.470.0runat.28062005.090805.20776 -ACPU=6 -ICPU=3  
-NO MMAP -LANG=QUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: N\_Geneseg\_16Dec04:\*

1: geneseqn1980s:\*\n2: geneseqn1990s:\*\n3: geneseqn2000s:\*\n4: geneseqn2001a:\*\n5: geneseqn2001b:\*\n6: geneseqn2002a:\*\n7: geneseqn2002b:\*\n8: geneseqn2003a:\*\n9: geneseqn2003b:\*\n10: geneseqn2003c:\*\n11: geneseqn2003d:\*\n12: geneseqn2004a:\*\n13: geneseqn2004b:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 495   | 88.7        | 1326   | 3  | AAA52135    |
| 2          | 495   | 88.7        | 1326   | 3  | AAA97036    |
| 3          | 495   | 88.7        | 2486   | 3  | AAA97037    |
| 4          | 495   | 88.7        | 2811   | 3  | AAA52134    |
| 5          | 221   | 39.6        | 1404   | 3  | AAA97065    |

|    |      |      |       |    |          |                     |
|----|------|------|-------|----|----------|---------------------|
| 6  | 221  | 39.6 | 1404  | 3  | AAA97040 | AAA97040 55KD i-an  |
| 7  | 221  | 39.6 | 1410  | 3  | AAA97089 | AAA97089 Synthetic  |
| 8  | 222  | 38.0 | 1404  | 3  | AAA52136 | AAA52136 55 kDa i-  |
| 9  | 212  | 38.0 | 1404  | 3  | AAA97038 | AAA97038 55KD i-an  |
| 10 | 212  | 38.0 | 1410  | 3  | AAA97060 | AAA97060 55KD i-an  |
| 11 | 121  | 21.7 | 123   | 3  | AAA97076 | AAA97076 GS synthe  |
| 12 | 88.5 | 15.9 | 921   | 4  | AB112251 | AB112251 Drosophila |
| 13 | 84.5 | 15.1 | 4355  | 12 | AD000957 | AD000957 Mouse hom  |
| 14 | 84.5 | 15.1 | 5216  | 12 | AD000955 | AD000955 Mouse hom  |
| 15 | 84.5 | 15.1 | 6056  | 6  | AB551293 | AB551293 Human RBM  |
| 16 | 84.5 | 15.1 | 7244  | 8  | ABX70916 | ABX70916 Novel hum  |
| 17 | 84.5 | 15.1 | 8589  | 6  | ADH48731 | ADH48731 NOV7 cod1  |
| 18 | 84.5 | 15.1 | 8957  | 10 | ADG75804 | ADG75804 Human pro  |
| 19 | 84.5 | 15.1 | 9921  | 10 | ADCS1659 | ADCS1659 DNA encod  |
| 20 | 84   | 15.1 | 2359  | 2  | AAV07901 | AAV07901 Cobra ven  |
| 21 | 83   | 14.9 | 94    | 3  | AAA97085 | AAA97085 GS synthe  |
| 22 | 83   | 14.9 | 3989  | 9  | ADA74090 | ADA74090 Equine Ia  |
| 23 | 81.5 | 14.6 | 1780  | 12 | ADG85575 | ADG85575 Human tum  |
| 24 | 81.5 | 14.6 | 1780  | 13 | ADG86680 | ADG86680 Human tum  |
| 25 | 81.5 | 14.6 | 1780  | 13 | ADG83429 | ADG83429 Human tum  |
| 26 | 81.5 | 14.6 | 1780  | 13 | ADG84203 | ADG84203 Human tum  |
| 27 | 81.5 | 14.6 | 1780  | 13 | ADG84667 | ADG84667 Human tum  |
| 28 | 80.5 | 14.4 | 783   | 8  | ACA25474 | ACA25474 Prokaryot  |
| 29 | 80   | 14.3 | 64125 | 13 | ABD33295 | ABD33295 Human can  |
| 30 | 79   | 14.2 | 2335  | 2  | AAV07897 | AAV07897 Cobra ven  |
| 31 | 79   | 14.2 | 2388  | 6  | ABQ94242 | ABQ94242 FLO11 gen  |
| 32 | 78   | 14.0 | 11009 | 6  | ABQ72907 | ABQ72907 Mouse lam  |
| 33 | 78   | 14.0 | 11009 | 6  | AAI70816 | AAI70816 Mouse lam  |
| 34 | 77.5 | 13.9 | 929   | 3  | AAI75097 | AAI75097 Trichoder  |
| 35 | 77.5 | 13.9 | 996   | 11 | ABD13214 | ABD13214 Pseudomon  |
| 36 | 77.5 | 13.9 | 1213  | 6  | ABK10638 | ABK10638 Pigmy rat  |
| 37 | 77.5 | 13.9 | 1545  | 11 | ABD12961 | ABD12961 Pseudomon  |
| 38 | 77.5 | 13.9 | 1722  | 13 | ADSL4692 | ADSL4692 Pseudomon  |
| 39 | 77.5 | 13.9 | 2589  | 11 | ABD13280 | ABD13280 Pseudomon  |
| 40 | 77   | 13.8 | 1340  | 2  | AAI78466 | AAI78466 Ankylosto  |
| 41 | 77   | 13.8 | 6330  | 6  | AB552998 | AB552998 Human CDN  |
| 42 | 77   | 13.8 | 11558 | 10 | ADJ38016 | ADJ38016 D melanog  |
| 43 | 77   | 13.8 | 11673 | 4  | AB116275 | AB116275 Drosophila |
| 44 | 76.5 | 13.7 | 3057  | 12 | AD000956 | AD000956 Human hom  |
| 45 | 76.5 | 13.7 | 6228  | 12 | ADG86896 | ADG86896 Human tum  |

## ALIGNMENTS

RESULT 1

ID AAA52135 standard; DNA; 1326 BP.

|    |    |   |   |
|----|----|---|---|
| XX | AC | AAA52135;   |   |
| XX | AC | AAA52135;   |   |
| XX | DT | 06-AUG-2003 (revised)   |   |
| XX | DT | 04-DEC-2000 (first entry)   |   |
| XX | DE | 48 kDa i-antigen gene.  |   |
| XX | XX | BTUL1, beta-tubulin; protein expression system; negative selection;   |   |
| XX | KW | pclitaxel sensitivity; cell surface; antigen; protozoa; ciliate;      |   |
| XX | KW | live vaccine; Ichthyophthirius multifiliis; immunobilization-antigen; |   |
| XX | KW | i-antigen; freshwater; fish; protozoacide; ds.                        |   |
| XX | OS | Ichthyophthirius multifiliis.   |   |
| XX | XX | Key   |   |
| XX | XX | Location/Qualifiers   |   |
| XX | XX | CDS   | 1..1326   |
| XX | XX | FT  | /*tag= a  |
| XX | XX | FT  | /trans_except= pos:82..84, aa:Gln                       |
| XX | XX | FT  | /codon= (seq: "TAA", aa:Gln) /product= 48 kDa i-antigen |
| XX | XX | FT  | /partial  |
| XX | XX | XX  | W0200046381-AL.   |
| XX | XX | XX  | 10-AUG-2000.  |

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 03:55:12 ; Search time 3372 Seconds  
(without alignments)  
1508.837 Million cell updates/sec

Title: US-09-196-161D-1

Perfect score: 558  
Sequence: 1 GAAQGEANGNPFAANNAAR.....PQGEAPGVQYFAAGAAAGV 105

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xlh  
-Q/cgml\_1/USPTO.spool\_h/US9196161/runat.28062005.090806.20783/app.query.fasta\_1.263  
-DB=GenBml -QFMT=faastap -SUFFIX=xge -MINMATCH=0.1 -LOOPT=0 -LOOEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pcr -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09196161 @CGML\_1.1.3731 @runat.28062005.090806.20783 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEOBJECT -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -MARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenBml:.\*  
1: gb\_ba:.\*  
2: gb\_hgt:.\*  
3: gb\_in:.\*  
4: gb\_cm:.\*  
5: gb\_ov:.\*  
6: gb\_pat:.\*  
7: gb\_ph:.\*  
8: gb\_pl:.\*  
9: gb\_dr:.\*  
10: gb\_ro:.\*  
11: gb\_sts:.\*  
12: gb\_sy:.\*  
13: gb\_un:.\*  
14: gb\_vl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description        |
|------------|-------|-------------|-----------|----|--------------------|
| 1          | 495   | 88.7        | 1249      | 3  | ICYMANT            |
| 2          | 495   | 88.7        | 2486      | 3  | AF140273 Ichthyoph |
| 3          | 212   | 38.0        | 3026      | 3  | AF344424 Ichthyoph |
| 4          | 194   | 34.8        | 1520      | 3  | AF405431 Ichthyoph |

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|-------------|
| 5          | 93    | 16.7        | 1644      | 3  | AF298862    |
| 6          | 93    | 16.7        | 2066      | 3  | GIASQAB     |
| 7          | 92.5  | 16.6        | 133860    | 9  | AF157709    |
| 8          | 91.5  | 16.4        | 1163      | 3  | AF312775    |
| 9          | 88.5  | 15.9        | 921       | 6  | CO587859    |
| 10         | 88.5  | 15.9        | 1041      | 3  | AY061512    |
| 11         | 87.5  | 15.7        | 186858    | 9  | AL356585    |
| 12         | 85.5  | 15.3        | 60090     | 1  | U30352      |
| 13         | 85    | 15.2        | 2730      | 3  | AY142126    |
| 14         | 85    | 15.2        | 37443     | 9  | AC144831    |
| 15         | 85    | 15.2        | 188644    | 9  | AC090518    |
| 16         | 85    | 15.2        | 198489    | 2  | AC067809    |
| 17         | 85    | 15.2        | 209706    | 2  | AC067885    |
| 18         | 84.5  | 15.1        | 5295      | 10 | BC060277    |
| 19         | 84.5  | 15.1        | 5528      | 10 | AK122377    |
| 20         | 84.5  | 15.1        | 5693      | 10 | BC036727    |
| 21         | 84.5  | 15.1        | 6056      | 6  | AX592784    |
| 22         | 84.5  | 15.1        | 6228      | 9  | AB011541    |
| 23         | 84.5  | 15.1        | 7244      | 6  | AR541895    |
| 24         | 84.5  | 15.1        | 8307      | 9  | AY280362    |
| 25         | 84.5  | 15.1        | 8589      | 6  | AX921022    |
| 26         | 84.5  | 15.1        | 9921      | 6  | BD185469    |
| 27         | 84    | 15.1        | 917       | 3  | AF312772    |
| 28         | 84    | 15.1        | 1084      | 3  | AF312771    |
| 29         | 84    | 15.1        | 1102      | 3  | AF312770    |
| 30         | 84    | 15.1        | 1639      | 11 | BV177181    |
| 31         | 83.5  | 15.0        | 174928    | 10 | AC121975    |
| 32         | 83    | 14.9        | 3475      | 3  | AF235028    |
| 33         | 83    | 14.9        | 3991      | 4  | AY082802    |
| 34         | 82.5  | 14.8        | 136620    | 2  | AC145502    |
| 35         | 82.5  | 14.8        | 233738    | 9  | AC007956    |
| 36         | 81.5  | 14.6        | 2965      | 1  | BC012775    |
| 37         | 81.5  | 14.6        | 2965      | 1  | AF099799    |
| 38         | 81.5  | 14.6        | 67849     | 2  | AC134685    |
| 39         | 81.5  | 14.6        | 110000    | 1  | BX571965    |
| 40         | 81.5  | 14.6        | 145247    | 9  | AF186192    |
| 41         | 81    | 14.5        | 5943      | 3  | AF354542    |
| 42         | 81    | 14.5        | 5943      | 5  | AF468050    |
| 43         | 81    | 14.5        | 13867     | 1  | AB011726    |
| 44         | 81    | 14.5        | 247196    | 2  | AC073822    |
| 45         | 80.5  | 14.4        | 2549      | 3  | AF202776    |

## ALIGNMENTS

| Result No. | Score | Query Match | Length DB | ID | Description        |
|------------|-------|-------------|-----------|----|--------------------|
| 1          | 495   | 88.7        | 1249      | 3  | ICYMANT            |
| 2          | 495   | 88.7        | 2486      | 3  | AF140273 Ichthyoph |
| 3          | 212   | 38.0        | 3026      | 3  | AF344424 Ichthyoph |
| 4          | 194   | 34.8        | 1520      | 3  | AF405431 Ichthyoph |

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 03:58:39 ; Search time 2653 Seconds  
(without alignments)  
1506.501 Million cell updates/sec

Title: US-09-196-161D-1  
Perfect score: 558  
Sequence: 1 GAAQGEANNGPFAANNAAR.....POGEAPGVQVFAAGAAAGV 105

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68473088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xlh  
-Q=/cgn2.1/USPTO.spool.h/US09196161/runat.28062005.090806.20794/app.query.fasta\_1.263  
-DB=EST -OPMT=fastap -SUFFIX=xet -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS-bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdd -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTPMT=ptc -NORR=ext -HEAPSIZ=500 -MINLEN=50 -MAXLEN=200000000  
-USBR=US09196161 @CGN 1.1 3437 @runat.28062005.090806.20794 -NCPU=6 -ICPU=3  
-NO\_MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
EST:.\*  
1: gb\_est1:.\*  
2: gb\_est2:.\*  
3: gb\_hic:.\*  
4: gb\_est3:.\*  
5: gb\_est4:.\*  
6: gb\_est5:.\*  
7: gb\_est6:.\*  
8: gb\_gsa1:.\*  
9: gb\_gsa2:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 194   | 34.8        | 523    | 5     | B0134970 INT1_2 D |
| 2          | 194   | 34.8        | 540    | 5     | B0134879 INT1_1 C |
| 3          | 194   | 34.8        | 560    | 5     | B0135128 INT1_3 F |
| 4          | 194   | 34.8        | 622    | 5     | B0134798 INT1_4 B |
| 5          | 194   | 34.8        | 630    | 5     | B0134905 INT1_1 F |
| 6          | 194   | 34.8        | 631    | 5     | B0134827 INT1_4 B |
| 7          | 194   | 34.8        | 687    | 5     | B0135168 INT1_4 B |
| 8          | 181.5 | 32.5        | 514    | 5     | B0134761 INT1_3 F |
| 9          | 180.5 | 32.3        | 661    | 5     | B0135189 INT1_4 D |

|      |       |      |      |   |          |
|------|-------|------|------|---|----------|
| 10   | 175   | 31.4 | 592  | 5 | B0134985 |
| C 11 | 144.5 | 25.9 | 419  | 5 | B0135036 |
| C 12 | 144   | 25.8 | 675  | 5 | B0135196 |
| C 13 | 140.5 | 25.2 | 502  | 5 | B0134889 |
| C 14 | 140.5 | 25.2 | 590  | 5 | B0135179 |
| C 15 | 140.5 | 25.2 | 602  | 5 | B0135164 |
| C 16 | 140.5 | 25.2 | 607  | 5 | B0134912 |
| C 17 | 140.5 | 25.2 | 658  | 5 | B0135057 |
| C 18 | 139.5 | 25.0 | 538  | 5 | B0134810 |
| C 19 | 139.5 | 25.0 | 539  | 5 | B0134821 |
| C 20 | 136.5 | 24.5 | 445  | 5 | B0134871 |
| C 21 | 133   | 23.8 | 150  | 5 | B0135114 |
| C 22 | 132   | 23.7 | 210  | 5 | B0134900 |
| C 23 | 89    | 15.9 | 711  | 6 | CD873037 |
| C 24 | 88.5  | 15.9 | 565  | 1 | A1516614 |
| C 25 | 88.5  | 15.9 | 563  | 4 | B1481638 |
| C 26 | 88.5  | 15.9 | 639  | 1 | A1515041 |
| C 27 | 88.5  | 15.9 | 694  | 6 | CD870573 |
| C 28 | 88.5  | 15.9 | 735  | 1 | AA952214 |
| C 29 | 88.5  | 15.9 | 876  | 8 | B2399503 |
| C 30 | 88    | 15.8 | 877  | 8 | CC376965 |
| C 31 | 87.5  | 15.7 | 478  | 5 | BQ810430 |
| C 32 | 87.5  | 15.7 | 569  | 2 | AW070824 |
| C 33 | 86.5  | 15.5 | 524  | 5 | BQ811391 |
| C 34 | 86.5  | 15.5 | 531  | 5 | BQ822580 |
| C 35 | 86.5  | 15.5 | 788  | 8 | B2385909 |
| C 36 | 86.5  | 15.5 | 919  | 1 | AL522459 |
| C 37 | 86.5  | 15.5 | 3140 | 3 | AK086911 |
| C 38 | 85.5  | 15.3 | 516  | 5 | BX37323  |
| C 39 | 85.5  | 15.3 | 1010 | 1 | AL559722 |
| C 40 | 85.5  | 15.3 | 1072 | 5 | BX396097 |
| C 41 | 85    | 15.2 | 558  | 2 | BE441419 |
| C 42 | 84.5  | 15.1 | 455  | 1 | AA619168 |
| C 43 | 84.5  | 15.1 | 459  | 7 | CN281628 |
| C 44 | 84.5  | 15.1 | 481  | 2 | AM676151 |
| C 45 | 84.5  | 15.1 | 602  | 7 | CF557698 |

## ALIGNMENTS

RESULT 1  
LOCUS B0134970 523 bp mRNA linear EST 22-APR-2002  
DEFINITION INT1\_2.D10.b1.A006.G5.trophont cDNA (INT1) Ichthyophthirius  
ACCESSION B0134970  
VERSION B0134970.1 GI:20261069  
KEYWORDS  
SOURCE  
ORGANISM  
EST  
Ichthyophthirius multifiliis  
Ichthyophthirius multifiliis  
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Ophryoglenina; Ichthyophthirius.  
1 (bases 1 to 523)  
Clark, T., Cordonier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,  
Dickerson, H., Lin, T.-L. and Pratt, L.H.  
An EST database for Ichthyophthirius multifiliis (G5 isolate)  
Unpublished (2002)  
Contact: Cordonier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmp@pratt.uga.edu

Sequences have been trimmed to exclude polyA, vector, and regions below paired quality 16. The threshold for highest quality sequence is 20.  
Seq primer: JEN REV  
High quality sequence stop: 508  
POLYA=No.  
Location/Qualifiers  
1..523  
/organism="Ichthyophthirius multifiliis"

FEATURES  
source

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OM protein - protein search, using sw model

Run on: June 30, 2005, 03:54:07 ; Search time 595 Seconds  
(without alignments)  
67.861 Million cell updates/sec

Title: US-09-196-161d-1

Sequence: 1 GAAGCAGANGOPFAANNAR.....PGCAPGVVFAAGAAAGV 105

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:  
1: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubppa/US07\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubppa/US11\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubppa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 558   | 100.0       | 442    | 17 | US-10-878-694-5   |
| 2          | 221   | 39.6        | 468    | 17 | US-10-878-694-6   |
| 3          | 87.5  | 15.7        | 3265   | 14 | US-10-184-644-257 |
| 4          | 87.5  | 15.7        | 3265   | 14 | US-10-184-644-257 |
| 5          | 87.5  | 15.7        | 3265   | 14 | US-10-063-685-69  |
| 6          | 85.5  | 15.3        | 914    | 9  | US-09-975-143-47  |
| 7          | 85.5  | 15.3        | 1076   | 14 | US-10-028-072-219 |
| 8          | 85.5  | 15.3        | 1076   | 14 | US-10-140-808-219 |
| 9          | 85.5  | 15.3        | 1076   | 14 | US-10-121-049-219 |
| 10         | 85.5  | 15.3        | 1076   | 14 | US-10-123-904-219 |
| 11         | 85.5  | 15.3        | 1076   | 14 | US-10-140-470-219 |

|    |      |      |      |    |                    |                   |
|----|------|------|------|----|--------------------|-------------------|
| 12 | 85.5 | 15.3 | 1076 | 14 | US-10-175-746-219  | Sequence 219, App |
| 13 | 85.5 | 15.3 | 1076 | 14 | US-10-176-918-219  | Sequence 219, App |
| 14 | 85.5 | 15.3 | 1076 | 14 | US-10-176-921-219  | Sequence 219, App |
| 15 | 85.5 | 15.3 | 1076 | 14 | US-10-137-865-219  | Sequence 219, App |
| 16 | 85.5 | 15.3 | 1076 | 14 | US-10-140-474-219  | Sequence 219, App |
| 17 | 85.5 | 15.3 | 1076 | 14 | US-10-142-431-219  | Sequence 219, App |
| 18 | 85.5 | 15.3 | 1076 | 14 | US-10-143-114-219  | Sequence 219, App |
| 19 | 85.5 | 15.3 | 1076 | 14 | US-10-142-419-219  | Sequence 219, App |
| 20 | 85.5 | 15.3 | 1076 | 14 | US-10-123-263-219  | Sequence 219, App |
| 21 | 85.5 | 15.3 | 1076 | 14 | US-10-142-423-219  | Sequence 219, App |
| 22 | 85.5 | 15.3 | 1076 | 14 | US-10-121-050-219  | Sequence 219, App |
| 23 | 85.5 | 15.3 | 1076 | 14 | US-10-141-755-219  | Sequence 219, App |
| 24 | 85.5 | 15.3 | 1076 | 14 | US-10-143-032-219  | Sequence 219, App |
| 25 | 85.5 | 15.3 | 1076 | 14 | US-10-123-108-219  | Sequence 219, App |
| 26 | 85.5 | 15.3 | 1076 | 14 | US-10-123-226-219  | Sequence 219, App |
| 27 | 85.5 | 15.3 | 1076 | 14 | US-10-123-261-219  | Sequence 219, App |
| 28 | 85.5 | 15.3 | 1076 | 14 | US-10-140-928-219  | Sequence 219, App |
| 29 | 85.5 | 15.3 | 1076 | 14 | US-10-140-928-219  | Sequence 219, App |
| 30 | 85.5 | 15.3 | 1076 | 14 | US-10-121-045-219  | Sequence 219, App |
| 31 | 85.5 | 15.3 | 1076 | 14 | US-10-123-292-219  | Sequence 219, App |
| 32 | 85.5 | 15.3 | 1076 | 14 | US-10-123-903-219  | Sequence 219, App |
| 33 | 85.5 | 15.3 | 1076 | 14 | US-10-124-819-219  | Sequence 219, App |
| 34 | 85.5 | 15.3 | 1076 | 14 | US-10-124-822-219  | Sequence 219, App |
| 35 | 85.5 | 15.3 | 1076 | 14 | US-10-140-925-219  | Sequence 219, App |
| 36 | 85.5 | 15.3 | 1076 | 14 | US-10-160-498-219  | Sequence 219, App |
| 37 | 85.5 | 15.3 | 1076 | 14 | US-10-124-824-219  | Sequence 219, App |
| 38 | 85.5 | 15.3 | 1076 | 14 | US-10-127-825A-219 | Sequence 219, App |
| 39 | 85.5 | 15.3 | 1076 | 14 | US-10-127-829A-219 | Sequence 219, App |
| 40 | 85.5 | 15.3 | 1076 | 14 | US-10-127-835A-219 | Sequence 219, App |
| 41 | 85.5 | 15.3 | 1076 | 14 | US-10-127-839A-219 | Sequence 219, App |
| 42 | 85.5 | 15.3 | 1076 | 14 | US-10-127-901A-219 | Sequence 219, App |
| 43 | 85.5 | 15.3 | 1076 | 14 | US-10-128-633A-219 | Sequence 219, App |
| 44 | 85.5 | 15.3 | 1076 | 14 | US-10-131-813A-219 | Sequence 219, App |
| 45 | 85.5 | 15.3 | 1076 | 14 | US-10-131-818A-219 | Sequence 219, App |

# ALIGNMENTS

RESULT 1  
US-10-878-694-5  
Sequence 5, Application US/10878694  
Publication No. US20050106164A1  
GENERAL INFORMATION:  
APPLICANT: GABRIG, Jacek  
APPLICANT: DICKERSON Jr., Harry W.  
APPLICANT: CLARK, Theodore G.  
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN  
FILE REFERENCE: 235, 00100101  
CURRENT APPLICATION NUMBER: US/10/878,694  
CURRENT FILING DATE: 2004-06-28  
PRIOR APPLICATION NUMBER: US/09/498,612  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/118,634  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: 60/122,372  
PRIOR FILING DATE: 1999-03-02  
PRIOR APPLICATION NUMBER: 60/124,905  
PRIOR FILING DATE: 1999-03-17  
PRIOR APPLICATION NUMBER: 60/131,121  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: PCT/US00/02966  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 442  
TYPE: PRT  
ORGANISM: Ichthyophthirius multifiliis  
US-10-878-694-5



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OM protein - protein search, using sw model

Run on: June 30, 2005, 03:22:56 ; Search time 29 Seconds  
(without alignments)  
270.281 Million cell updates/sec

Title: US-09-196-161D-1

Sequence: 1 GAAGGANGNGPFAANNAR.....PGGAPGVVFAAGAAAGV 105

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 0%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/prodata/1/iaa/5A COMB pep: \*  
2: /cgn2\_6/prodata/1/iaa/5B COMB pep: \*  
3: /cgn2\_6/prodata/1/iaa/6A COMB pep: \*  
4: /cgn2\_6/prodata/1/iaa/6B COMB pep: \*  
5: /cgn2\_6/prodata/1/iaa/PCTUS COMB pep: \*  
6: /cgn2\_6/prodata/1/iaa/backfile1 pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description          |
|------------|-------|-------------|--------|-------|----------------------|
| 1          | 84    | 15.1        | 613    | 4     | US-09-026-001A-10    |
| 2          | 84    | 15.1        | 621    | 4     | US-09-026-001A-18    |
| 3          | 78.5  | 14.1        | 605    | 4     | US-09-976-594-616    |
| 4          | 78    | 14.0        | 3635   | 4     | US-09-845-583A-2     |
| 5          | 77.5  | 13.9        | 862    | 4     | US-09-252-991A-28455 |
| 6          | 77.5  | 13.9        | 3647   | 4     | US-09-949-016-10932  |
| 7          | 77    | 13.8        | 314    | 2     | US-08-460-309-19     |
| 8          | 77    | 13.8        | 314    | 2     | US-08-125-077-19     |
| 9          | 77    | 13.8        | 424    | 1     | US-08-419-414-2      |
| 10         | 77    | 13.8        | 1551   | 4     | US-09-949-016-6785   |
| 11         | 76    | 13.6        | 1694   | 4     | US-09-560-885A-12    |
| 12         | 76    | 13.6        | 1725   | 4     | US-09-560-885A-10    |
| 13         | 75.5  | 13.5        | 2508   | 4     | US-09-627-650B-7     |
| 14         | 75.5  | 13.5        | 2508   | 4     | US-09-436-063C-7     |
| 15         | 75.5  | 13.5        | 2544   | 4     | US-09-627-650B-3     |
| 16         | 75.5  | 13.5        | 2544   | 4     | US-09-436-063C-3     |
| 17         | 75.5  | 13.5        | 2601   | 4     | US-09-627-650B-9     |
| 18         | 75.5  | 13.5        | 2601   | 4     | US-09-436-063C-9     |
| 19         | 75    | 13.4        | 169    | 2     | US-08-460-309-20     |
| 20         | 75    | 13.4        | 169    | 2     | US-08-125-077-20     |
| 21         | 75    | 13.4        | 1111   | 1     | US-08-317-450B-15    |
| 22         | 75    | 13.4        | 1111   | 3     | US-08-800-593-15     |
| 23         | 75    | 13.4        | 1172   | 4     | US-09-560-385A-28    |
| 24         | 75    | 13.4        | 1172   | 4     | US-09-560-385A-32    |
| 25         | 75    | 13.4        | 1193   | 3     | US-08-317-450B-13    |
| 26         | 75    | 13.4        | 1193   | 3     | US-08-800-593-13     |
| 27         | 75    | 13.4        | 1193   | 4     | US-09-560-385A-26    |

|    |      |      |      |   |                     |                   |
|----|------|------|------|---|---------------------|-------------------|
| 28 | 75   | 13.4 | 1193 | 4 | US-09-560-385A-30   | Sequence 30, Appl |
| 29 | 74   | 13.3 | 1461 | 4 | US-10-142-231-86    | Sequence 86, Appl |
| 30 | 72.5 | 13.0 | 530  | 4 | US-09-949-016-10781 | Sequence 10781, A |
| 31 | 72.5 | 13.0 | 909  | 4 | US-09-949-016-6370  | Sequence 6370, Ap |
| 32 | 72   | 12.9 | 234  | 4 | US-09-130-491-12    | Sequence 12, Appl |
| 33 | 72   | 12.9 | 467  | 3 | US-09-086-483A-6    | Sequence 6, Appl  |
| 34 | 72   | 12.9 | 467  | 4 | US-09-580-212-6     | Sequence 6, Appl  |
| 35 | 72   | 12.9 | 467  | 4 | US-09-769-402-6     | Sequence 6, Appl  |
| 36 | 72   | 12.9 | 468  | 3 | US-09-013-895A-2    | Sequence 2, Appl  |
| 37 | 72   | 12.9 | 468  | 4 | US-09-565-918-2     | Sequence 2, Appl  |
| 38 | 72   | 12.9 | 468  | 4 | US-09-448-868-2     | Sequence 2, Appl  |
| 39 | 72   | 12.9 | 468  | 4 | US-09-949-016-6423  | Sequence 6423, Ap |
| 40 | 72   | 12.9 | 991  | 4 | US-09-949-016-7768  | Sequence 7768, Ap |
| 41 | 71.5 | 12.8 | 1572 | 4 | US-09-562-702A-32   | Sequence 32, Appl |
| 42 | 71.5 | 12.8 | 1572 | 4 | US-09-561-818A-28   | Sequence 28, Appl |
| 43 | 71.5 | 12.8 | 1605 | 4 | US-09-562-702A-30   | Sequence 30, Appl |
| 44 | 71.5 | 12.8 | 1605 | 4 | US-09-561-818A-26   | Sequence 26, Appl |
| 45 | 71.5 | 12.8 | 2088 | 4 | US-09-548-372D-13   | Sequence 13, Appl |

# ALIGNMENTS

RESULT 1  
US-09-026-001A-10  
Sequence 10, Application US/09026001A  
Patent No. 6413760  
GENERAL INFORMATION:  
APPLICANT: Boonhoo, Amechand  
APPLICANT: Seehra, Jasbir  
APPLICANT: Shaw, Gray  
APPLICANT: Sako, Diane  
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM  
TITLE OF INVENTION: THERAPEUTIC USES THEREOF  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/026,001A  
FILING DATE: 18-FEB-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 613 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-026-001A-10  
Query Match 15.1%, Score 84, DB 4, Length 613;  
Best Local Similarity 29.2%, Pred. No. 0.8;  
Matches 28, Conservative 10, Mismatches 36, Indels 22, Gaps 5;  
11 GPFANNMARGICVQCQINRVSVMNAG----DLATLATQCSTQCCTGTALDDGTVDDVD 66

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OM protein - protein search, using sw model

Run on: June 30, 2005, 02:04:50 ; Search time 86 Seconds  
(without alignments)  
472.207 Million cell updates/sec

Title: US-09-196-161D-1

Perfect score: 558  
Sequence: 1 GAAQGEAMNGQPFANNAAR.....PQGAFGVYFAAGAAAGV 105

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: A\_Geneseq\_16Dec04:\*

1: geneseqp19808:\*\n2: geneseqp19808:\*\n3: geneseqp20008:\*\n4: geneseqp20018:\*\n5: geneseqp20028:\*\n6: geneseqp20038:\*\n7: geneseqp20038:\*\n8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 558   | 100.0       | 409    | 3  | AAB25889    |
| 2          | 558   | 100.0       | 442    | 3  | AA97176     |
| 3          | 558   | 100.0       | 442    | 3  | AA97176     |
| 4          | 297   | 53.2        | 89     | 3  | AAB25862    |
| 5          | 261   | 46.8        | 83     | 3  | AAB25861    |
| 6          | 258   | 46.2        | 89     | 3  | AAB25863    |
| 7          | 221   | 39.6        | 468    | 3  | AA97177     |
| 8          | 221   | 39.6        | 468    | 3  | AAB25882    |
| 9          | 221   | 39.6        | 468    | 3  | AAB25880    |
| 10         | 139   | 24.9        | 76     | 3  | AAB25885    |
| 11         | 119   | 21.3        | 69     | 3  | AAB25864    |
| 12         | 102   | 18.3        | 72     | 3  | AAB25888    |
| 13         | 91    | 16.3        | 1755   | 8  | ADP31446    |
| 14         | 89    | 15.9        | 72     | 3  | AAB25865    |
| 15         | 86    | 15.4        | 1464   | 6  | ADP31437    |
| 16         | 85.5  | 15.3        | 1076   | 6  | ABU6845     |
| 17         | 84.5  | 15.1        | 1450   | 8  | ADDO01059   |
| 18         | 84.5  | 15.1        | 1737   | 8  | ADDO01057   |
| 19         | 84.5  | 15.1        | 1774   | 8  | ABG69800    |
| 20         | 84.5  | 15.1        | 2778   | 7  | ADCS1660    |
| 21         | 84.5  | 15.1        | 2769   | 7  | ADG75733    |
| 22         | 84.5  | 15.1        | 2854   | 5  | ADH48732    |
| 23         | 84.5  | 15.1        | 613    | 2  | AAW73009    |
| 24         | 84    | 15.1        | 621    | 2  | AAW73013    |
| 25         | 84    | 15.1        | 621    | 2  | AAW73013    |

|    |      |      |      |   |          |
|----|------|------|------|---|----------|
| 26 | 83.5 | 15.0 | 70   | 3 | AAB25887 |
| 27 | 83.5 | 15.0 | 7339 | 6 | AA016358 |
| 28 | 83   | 14.9 | 13   | 3 | AAB25898 |
| 29 | 83   | 14.9 | 70   | 3 | AAB25884 |
| 30 | 83   | 14.9 | 1190 | 6 | ADA74091 |
| 31 | 83   | 14.9 | 1849 | 8 | ADP30752 |
| 32 | 82   | 14.7 | 472  | 8 | ADP31222 |
| 33 | 82   | 14.7 | 750  | 8 | ADP31131 |
| 34 | 81.5 | 14.6 | 525  | 8 | ADP31227 |
| 35 | 80.5 | 14.4 | 261  | 6 | ADU21604 |
| 36 | 80.5 | 14.4 | 1587 | 8 | ADP30579 |
| 37 | 80   | 14.3 | 320  | 8 | ADP31607 |
| 38 | 80   | 14.3 | 320  | 8 | ADP31649 |
| 39 | 79.5 | 14.2 | 531  | 8 | ADP31696 |
| 40 | 79.5 | 14.2 | 337  | 8 | ADP31387 |
| 41 | 79   | 14.2 | 5397 | 8 | ADP31068 |
| 42 | 78.5 | 14.1 | 605  | 8 | ADL12887 |
| 43 | 78   | 14.0 | 348  | 8 | ADP30985 |
| 44 | 78   | 14.0 | 2468 | 8 | ADP30947 |
| 45 | 78   | 14.0 | 3635 | 5 | AB881589 |

## ALIGNMENTS

|   |  |
|---|--|
| RESULT 1  |  |
| AAB25889  |  |
| ID AAB25889 standard; protein; 409 AA.                                      |  |
| XX  |  |
| AC AAB25889;  |  |
| XX  |  |
| DT 18-DEC-2000 (first entry)  |  |
| XX  |  |
| DE IAG48 (GI) surface protein amino acid sequence.                          |  |
| XX  |  |
| KW Immobilisation antigen; i-antigen; ichthyophthiriasis; vaccine;          |  |
| KM white spot disease; freshwater fish; immune response; infection control. |  |
| XX  |  |
| OS Ichthyophthirius multifiliis.  |  |
| XX  |  |
| PN W0200046373-A1.  |  |
| XX  |  |
| PD 10-AUG-2000.   |  |
| XX  |  |
| PF 04-FEB-2000; 2000WO-US002962.  |  |
| XX  |  |
| PR 04-FEB-1999; 99US-0118634P.  |  |
| PR 02-MAR-1999; 99US-0122372P.  |  |
| PR 17-MAR-1999; 99US-0124505P.  |  |
| PR 27-APR-1999; 99US-0131121P.  |  |
| XX  |  |
| PA (UYGE-) UNIV GEORGIA RES FOUND INC.                                      |  |
| PA (CORR.) CORNELL RES FOUND INC.   |  |
| PA (CLAR.) CLARK T G.   |  |
| PA (DICK/) DICKERSON H W.   |  |
| PA (LINT/) LINT T.  |  |
| XX  |  |
| PI Clark TG, Dickerson HW, Lint T;  |  |
| XX  |  |
| DR WPI; 2000-506071/45.   |  |
| XX  |  |
| PT Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius   |  |
| PT multifiliis, useful for prophylaxis and treatment of ichthyophthirius    |  |
| PT infection in fish.   |  |
| XX  |  |
| PS Disclosure; Fig 8; 144pp; English.                                       |  |
| XX  |  |
| CC This invention relates to novel i-antigen polypeptide sequences. I-      |  |
| CC antigens or immobilisation antigens as common to a variety of            |  |
| CC hymenostomatid ciliates and their expression varies in response to       |  |
| CC environmental stimuli. This invention relates to i-antigen in            |  |
| CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite  |  |
| CC of freshwater fish causing Ichthyophthiriasis or white spot disease. The |  |



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OM protein - protein search, using sw model

Run on: June 30, 2005, 03:41:16 ; Search time 25 Seconds  
(without alignments)  
404.110 Million cell updates/sec

Title: US-09-196-161d-1

Perfect score: 558

Sequence: 1 GAAQGEANGNOPFAANNAR.....PGSEAPGVYFAAGAAAGV 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79: \*  
2: PIR1: \*  
3: PIR2: \*  
4: PIR3: \*  
5: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID     | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 558   | 100.0       | 395    | 2 A46031  | immobilization sur |
| 2          | 93    | 16.7        | 677    | 2 C42125  | trophozoite cyste  |
| 3          | 84.5  | 15.1        | 1737   | 2 T00209  | MEGF8 protein - hu |
| 4          | 78    | 14.0        | 596    | 2 A45664  | variant-specific s |
| 5          | 78    | 14.0        | 3635   | 2 T10053  | laminin alpha-5 ch |
| 6          | 77.5  | 13.9        | 573    | 2 D83130  | probable iron-sulf |
| 7          | 77    | 13.8        | 1372   | 2 T25933  | hypothetical prote |
| 8          | 77    | 13.8        | 3712   | 2 S18253  | laminin alpha-1 ch |
| 9          | 75.5  | 13.5        | 713    | 2 A35502  | major surface-labe |
| 10         | 75    | 13.4        | 1193   | 2 A44018  | laminin B2c chain  |
| 11         | 75    | 13.4        | 3084   | 1 MMSA    | laminin alpha-1 ch |
| 12         | 72.5  | 13.0        | 398    | 1 S24802  | polyferredoxin 6x2 |
| 13         | 72.5  | 13.0        | 2225   | 2 T26063  | hypothetical prote |
| 14         | 72    | 12.9        | 109    | 2 S18323  | chryoglobulin - bu |
| 15         | 72    | 12.9        | 610    | 2 JCT530  | vascular apoptosis |
| 16         | 71    | 12.7        | 1713   | 2 A55347  | adhesive ligand ep |
| 17         | 70.5  | 12.6        | 289    | 2 T25682  | hypothetical prote |
| 18         | 70.5  | 12.6        | 1607   | 1 MMSB2   | laminin gamma-1 ch |
| 19         | 70    | 12.5        | 485    | 2 S36772  | B-selectin - bovin |
| 20         | 69.5  | 12.5        | 2824   | 2 T22759  | hypothetical prote |
| 21         | 69    | 12.4        | 610    | 2 JCT8056 | halysae - Gloydin  |
| 22         | 69    | 12.4        | 1557   | 2 T28811  | hypothetical prote |
| 23         | 68.5  | 12.3        | 371    | 2 C97559  | conserved hypotet  |
| 24         | 68.5  | 12.3        | 425    | 2 AH2779  | protein P11C7.3 [l |
| 25         | 68.5  | 12.3        | 431    | 2 C89753  | ccog protein - Par |
| 26         | 68.5  | 12.3        | 484    | 2 S77602  | subtilisin-like pr |
| 27         | 68.5  | 12.3        | 962    | 2 JCT5571 | subtilisin-like pr |
| 28         | 68.5  | 12.3        | 969    | 1 A39490  | subtilisin-like pr |
| 29         | 68.5  | 12.3        | 975    | 2 JCT5570 | subtilisin-like pr |

|    |      |      |      |          |                    |
|----|------|------|------|----------|--------------------|
| 30 | 68.5 | 12.3 | 1280 | 2 A39117 | 170K lectin precur |
| 31 | 68.5 | 12.3 | 1695 | 2 T15881 | hypothetical prote |
| 32 | 68.5 | 12.3 | 2014 | 2 T21560 | hypothetical prote |
| 33 | 68   | 12.2 | 738  | 2 S40992 | hypothetical prote |
| 34 | 68   | 12.2 | 739  | 2 B88553 | protein K04H4.2b l |
| 35 | 67.5 | 12.1 | 496  | 2 F87423 | ferredoxin, probab |
| 36 | 67.5 | 12.1 | 932  | 2 I52527 | PACSA4 - mouse (fr |
| 37 | 67   | 12.0 | 294  | 2 T21668 | hypothetical prote |
| 38 | 67   | 12.0 | 314  | 2 I37383 | PAS soluble protei |
| 39 | 67   | 12.0 | 335  | 2 A40036 | apoptosis-mediati  |
| 40 | 67   | 12.0 | 439  | 2 A36385 | surface antigen se |
| 41 | 67   | 12.0 | 510  | 2 AD1554 | D-alanine-activat  |
| 42 | 67   | 12.0 | 563  | 2 AB3417 | electron-transferr |
| 43 | 67   | 12.0 | 1639 | 1 MMRFB2 | laminin gamma-1 ch |
| 44 | 67   | 12.0 | 1827 | 2 T34288 | hypothetical prote |
| 45 | 67   | 12.0 | 3075 | 2 S14458 | laminin alpha-1 ch |

#### ALIGNMENTS

RESULT 1  
A46031  
immobilization surface I-antigen precursor - Ichthyophthirius multifiliis (fragment)  
C/Species: Ichthyophthirius multifiliis  
C/Date: 29-Sep-1999 #sequence\_revision 29-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: A46031  
R/Clark, T.G.; McGraw, R.A.; Dickerson, H.W.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6363-6367, 1992  
A/Title: Developmental expression of surface antigen genes in the parasitic ciliate Ichth  
A/Reference number: A46031; MIMD:92335298; PMID:1631132  
A/Accession: A46031  
A/Molecule type: mRNA; protein  
A/Residues: 1-395 <CLAS>  
A/Cross-references: UNIPROT:Q27208; GB:M92907; NID:q3628568; PIDN:AC36158.1; PID:q362856  
F/2-395/Product: immobilization surface I-antigen #status experimental <MNT>  
P/156,191,245,281/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 558; DB 2; Length 395;  
Best Local Similarity 100.0%; Pred. No. 1.5e-46;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAQGEANGNOPFAANNARGICVPCQINRVGSYTNAGLATLATTCSTQCPGTALDDG 60  
DB 37 GAAQGEANGNOPFAANNARGICVPCQINRVGSYTNAGLATLATTCSTQCPGTALDDG 96  
QY 61 VWDVDFRSAAQCVKCKPNFYNGSPQGEAPGVYFAAGAAAGV 105  
DB 97 VWDVDFRSAAQCVKCKPNFYNGSPQGEAPGVYFAAGAAAGV 141

RESULT 2  
C42125  
trophozoite cysteine-rich surface antigen 72 - Giardia lamblia (fragment)  
N/Alternate names: CRP72  
C/Species: Giardia lamblia  
C/Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004  
C/Accession: C42125  
R/Adam, R.D.; Yang, Y.M.; Nash, T.B.  
Mol. Cell. Biol. 12, 1194-1201, 1992  
A/Title: The cysteine-rich protein gene family of Giardia lamblia: loss of the CRP170 ger  
A/Reference number: A42125; MIMD:92186850; PMID:1545800  
A/Molecule type: DNA  
A/Residues: 1-677 <ADA>  
A/Cross-references: UNIPROT:Q7M3R4; GB:M83934; NID:q159123  
A/Experimental source: trophozoites  
A/Note: sequence extracted from NCBI backbone (NCBIN:88443; NCBI:88444); this ORF is not